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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 16, 2003, 16:40:32 | Search time: 18:24:3 seconds

(without alignments)
56,562 million cell updates/sec

Perfect score: 23 MS-09-K6-017n-2A

Sequence: 1 MFLQI 5

Scoring table: BL05UM62 Gap-p 10.0 , Gap-wt 0.5

Searched: 671580 seqs, 20647115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SPTRIMBL_211,*

1: sp_archaea,*

2: sp_bacteria,*

3: sp_fungi,*

4: sp_human,*

5: sp_invertebrate,*

6: sp_mammal,*

7: sp_mhc,*

8: sp_organelle,*

9: sp_phage,*

10: sp_plant,*

11: sp_rhodent,*

12: sp_virus,*

13: sp_vertebrate,*

14: sp_unclassified,*

15: sp_virus,*

16: sp_bacteriap,*

17: sp_archeap,*

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15:	sp_virus,*
16:	sp_bacteriap,*
17:	sp_archeap,*

ALIGNMENTS

RESULT 1	Q9BG35	PRELIMINARY:	PRT;	25 AA.
	ID: Q9BG35			
	AC: Q9BG35;			
	DT: 01-JUN-2001 (TREMBLE); 17, Created)			
	DT: 01-JUN-2001 (TREMBLE); 17, last sequence update)			
	DT: 01-JPC-2001 (TREMBLE); 19, last annotation update)			
	DE: ATP synthase beta subunit (Fragment).			
	OS: Macaca fasciata (Crab-eating macaque) (Cynomolgus monkey).			
	OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	OC: Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
	OC: Cercopithecinae; Macaca.			
	OX: NCB_1 TAXID=954;			
RN: [1]				
PP: SEQUENCE FROM N/A				
RX: MEDLINE-2410652; PubMed-11156996;				
Schmitz, J., Oehne, M., Zischler, H.				
R1: SINE insertions in Cladistic Analyses and the Phylogenetic				
RT: Affiliations of <i>Tarsius bancanus</i> to other primates.;				
RL: EMBL; AF278735; AAC13310.1; -.				
DR: FT NON-TER 1				
PT: 25 AA;	25 AA;	25 AA;	25 AA;	25 AA;
SG: SEQUENCE				
Query	Query	Description		
No.	Match	Lengt	DB	ID
1	23	100.0	25	6 Q9BG35
2	23	100.0	25	6 Q9BG34
3	23	100.0	17	Q9YK14
4	23	100.0	18	Q9YK14
5	23	100.0	151	4 Q9PONC
6	23	100.0	156	4 Q9UJF8
7	23	100.0	157	17 Q9F55E
8	23	100.0	158	4 Q9UD77
9	23	100.0	159	4 Q9UJF6
10	23	100.0	161	4 Q9UJF9
11	23	100.0	168	10 Q9LR06
12	23	100.0	173	10 Q9FJF3
13	23	100.0	195	4 Q9WV17
14	23	100.0	196	10 Q94T55
15	23	100.0	196	13 Q9YU8
16	23	100.0	236	16 Q9C27A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Lengt	DB	ID	Description
1	23	100.0	25	6 Q9BG35	C9EJ5 macaca fasciata	
2	23	100.0	25	6 Q9BG34	O9bj4 pygathrix nigeriana aequipotrix p. galiiwa oriza sativa	
3	23	100.0	17	Q9YK14	Q9fuj2 homo sapien	
4	23	100.0	18	Q9YK14	Q9Uj28 homo sapien	
5	23	100.0	151	4 Q9PONC	Q9B577 arachaeoqib	
6	23	100.0	156	4 Q9UJF8	Q9bj7 homo sapien	
7	23	100.0	157	17 Q9F55E	Q9Uj6 home sapien	
8	23	100.0	158	4 Q9UD77	Q9Uj20 homo sapien	
9	23	100.0	159	4 Q9UJF6	Q9lr06 arachidopsis	
10	23	100.0	161	4 Q9UJF9	Q9fjp3 arachidopsis	
11	23	100.0	168	10 Q9LR06	Q9YU8 icelaurus	
12	23	100.0	173	10 Q9FJF3	Q9YU8 listeria in	
13	23	100.0	195	4 Q9WV17	Q9YU8 listeria mo	
14	23	100.0	196	10 Q94T55	Q9YU8 listeria in	
15	23	100.0	196	13 Q9YU8	Q9YU8 listeria mo	
16	23	100.0	236	16 Q9C27A	Q9C27A listeria in	

RESULT 2

SEQUENCE FROM N/A

PP: SEQUENCE FROM N/A

RX: MEDLINE-2410652; PubMed-11156996;

Schmitz, J., Oehne, M., Zischler, H.

R1: SINE insertions in Cladistic Analyses and the Phylogenetic

RT: Best Local Similarity 100.0%; Ped. No. 35;

RT: Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RL: EMBL; AF278735; AAC13310.1; -.

DR: NCBI_1 TAXID=954;

FT: NON-TER 1

PT: 25 AA;

SG: SEQUENCE

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